Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:12:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084779.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3084779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:12:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,699,622
Mapped reads	1,543,337 / 90.8%
Unmapped reads	156,285 / 9.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,675 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	64,133 / 3.77%
Duplication rate	3.37%
Clipped reads	658,735 / 38.76%

2.2. ACGT Content

Number/percentage of A's	28,726,999 / 27.7%
Number/percentage of C's	19,237,121 / 18.55%
Number/percentage of T's	32,655,957 / 31.49%
Number/percentage of G's	23,037,424 / 22.22%
Number/percentage of N's	40,206 / 0.04%
GC Percentage	40.77%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.2878

2.4. Mapping Quality

Mean Mapping Quality	46.9

2.5. Mismatches and indels

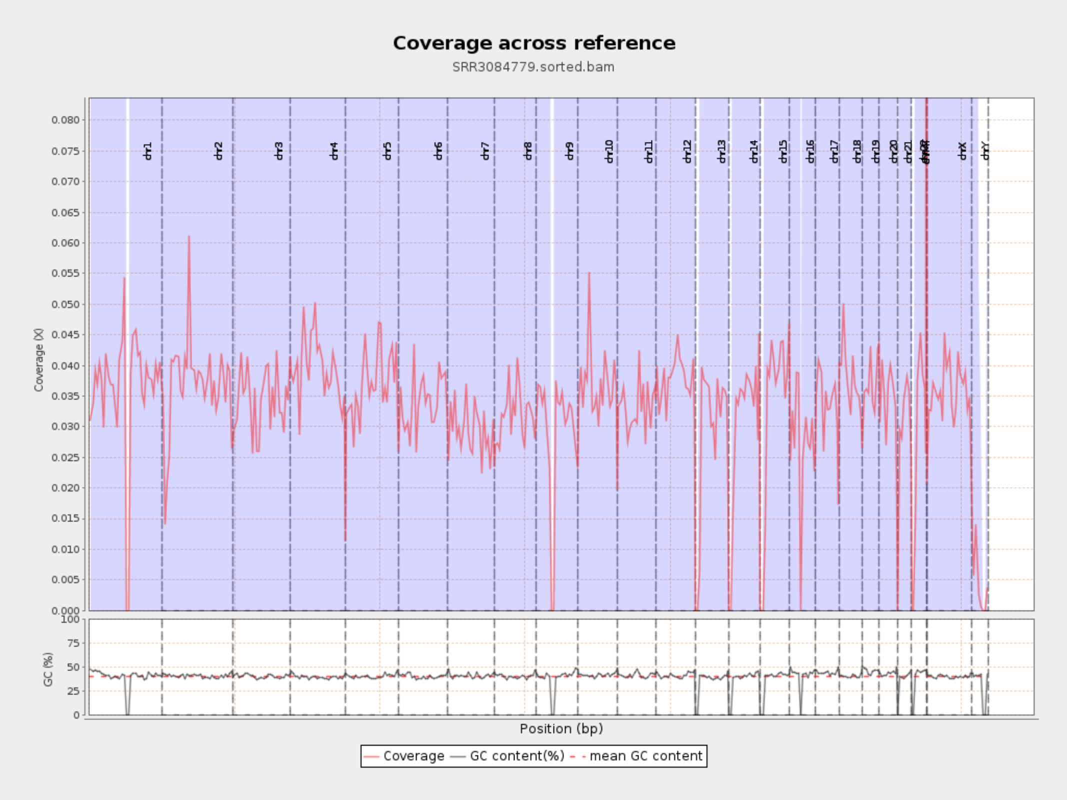
General error rate	0.88%
Mismatches	893,645
Insertions	8,103
Mapped reads with at least one insertion	0.52%
Deletions	24,637
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.63%

2.6. Chromosome stats

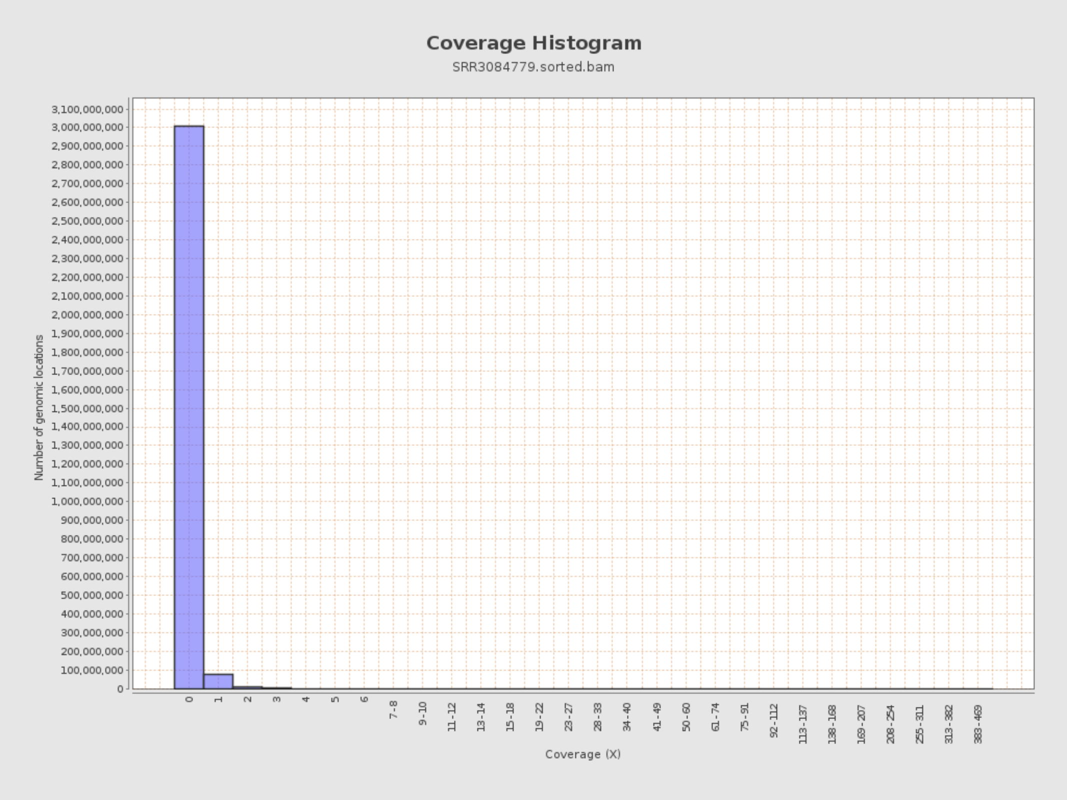
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9015468	0.0362	0.4397
chr2	243199373	8972626	0.0369	0.3479
chr3	198022430	6787758	0.0343	0.2076
chr4	191154276	7555167	0.0395	0.2334
chr5	180915260	6676375	0.0369	0.2171
chr6	171115067	5822106	0.034	0.2397
chr7	159138663	4706927	0.0296	0.2757

chr8	146364022	4670495	0.0319	0.3404
chr9	141213431	4097263	0.029	0.2742
chr10	135534747	5015138	0.037	0.2757
chr11	135006516	4442495	0.0329	0.2663
chr12	133851895	5067736	0.0379	0.2216
chr13	115169878	3290240	0.0286	0.1921
chr14	107349540	3170018	0.0295	0.2098
chr15	102531392	3344840	0.0326	0.2076
chr16	90354753	2456112	0.0272	0.2119
chr17	81195210	2728864	0.0336	0.2208
chr18	78077248	2996320	0.0384	0.6364
chr19	59128983	2176851	0.0368	0.327
chr20	63025520	2181713	0.0346	0.2186
chr21	48129895	1407585	0.0292	0.2021
chr22	51304566	1383066	0.027	0.1824
chrMT	16571	6139	0.3705	0.6591
chrX	155270560	5506906	0.0355	0.2343
chrY	59373566	259878	0.0044	0.1048

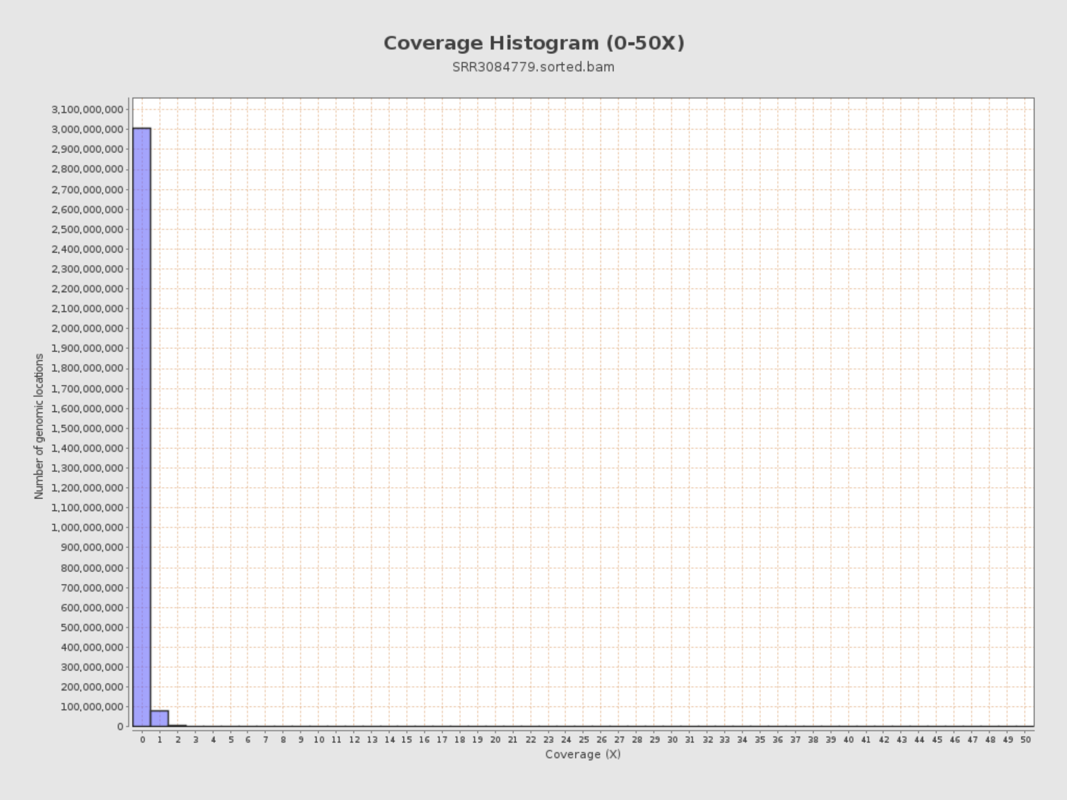
3. Results : Coverage across reference



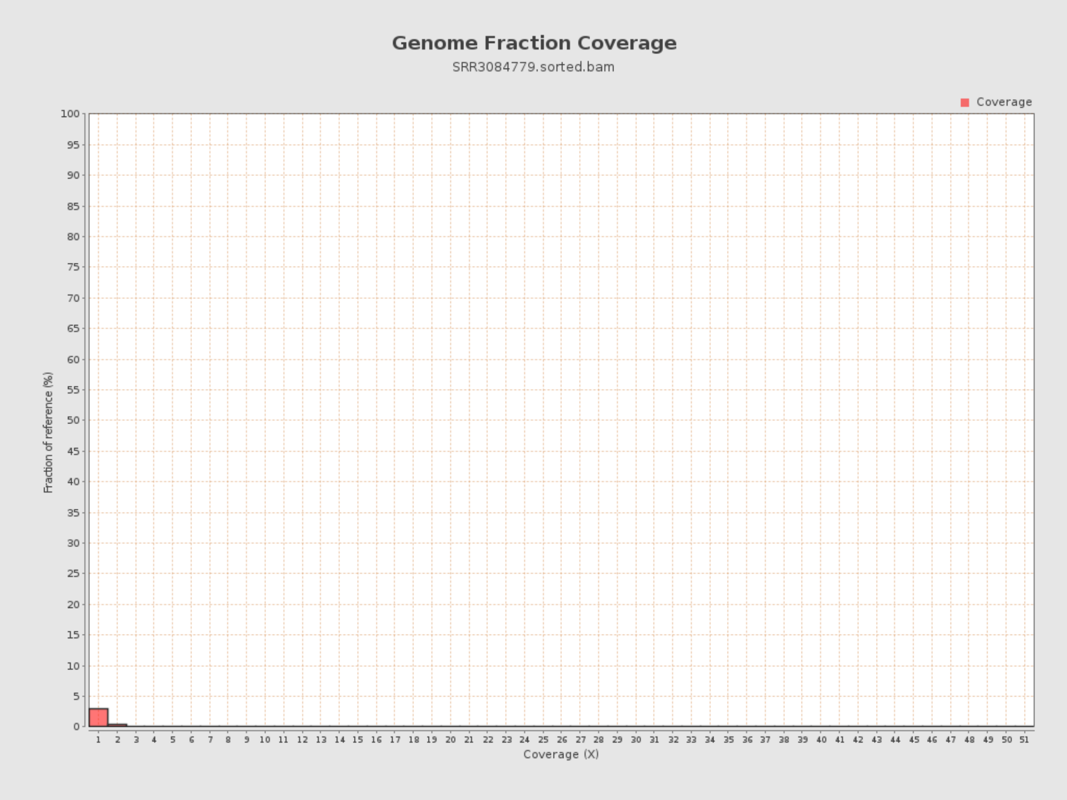
4. Results : Coverage Histogram



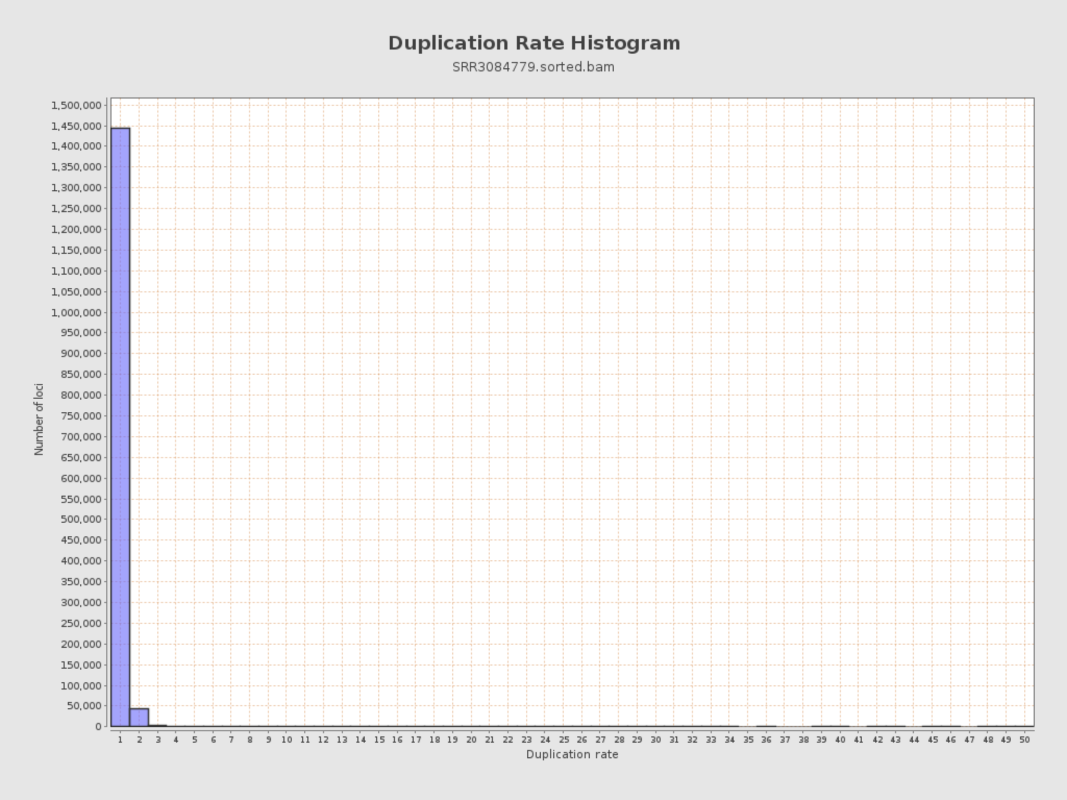
5. Results : Coverage Histogram (0-50X)



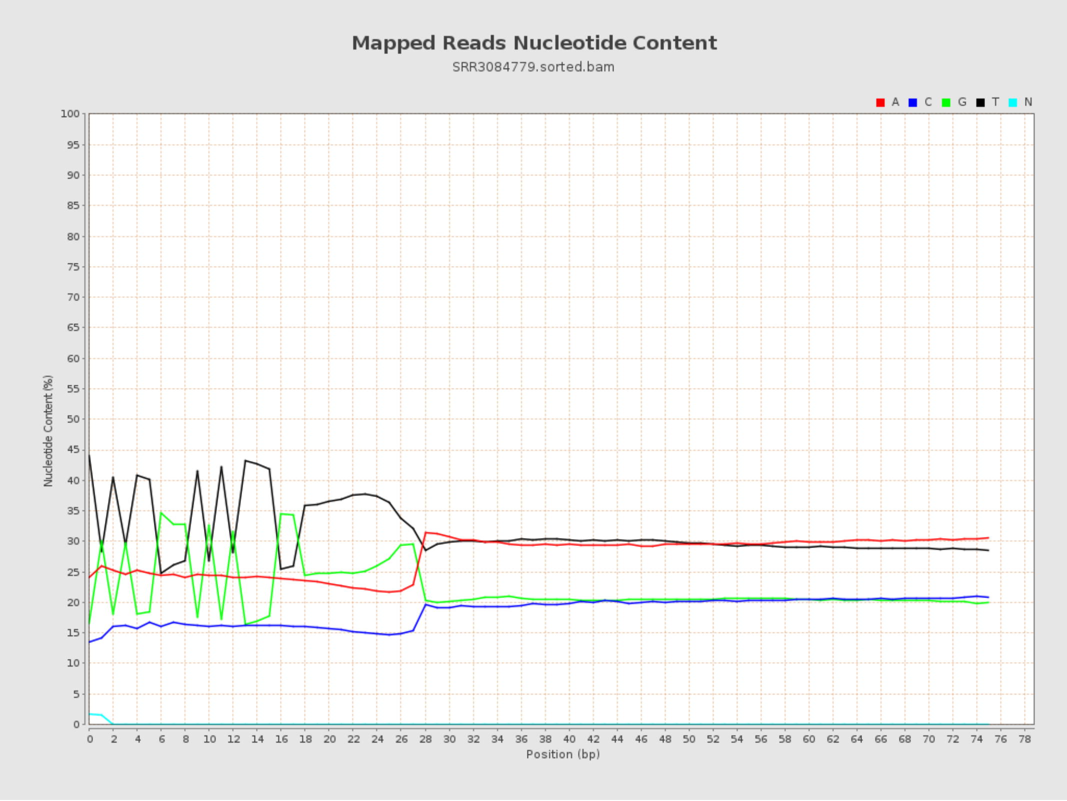
6. Results : Genome Fraction Coverage



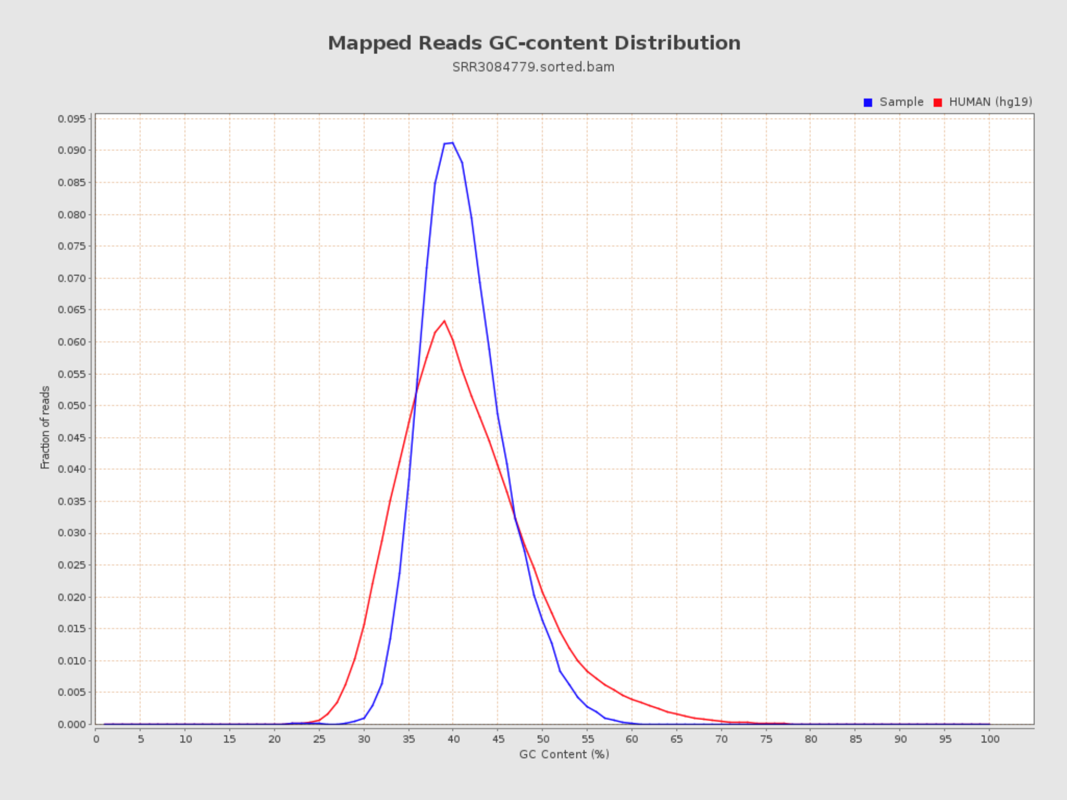
7. Results : Duplication Rate Histogram



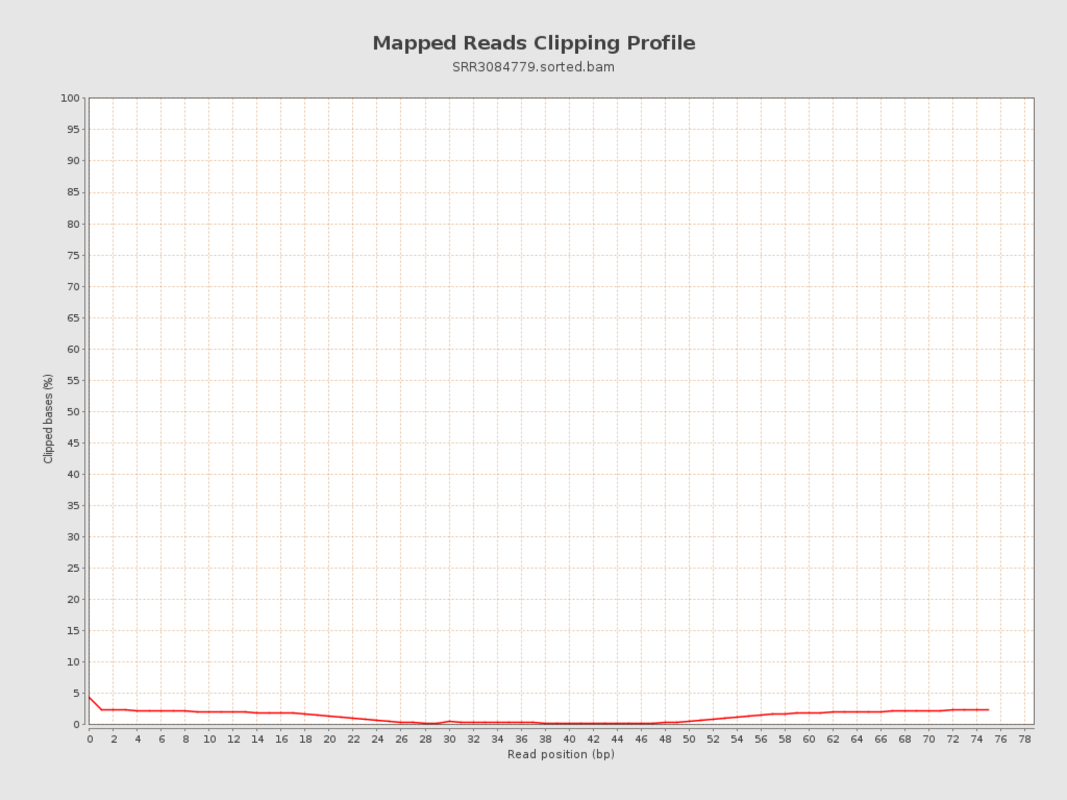
8. Results : Mapped Reads Nucleotide Content



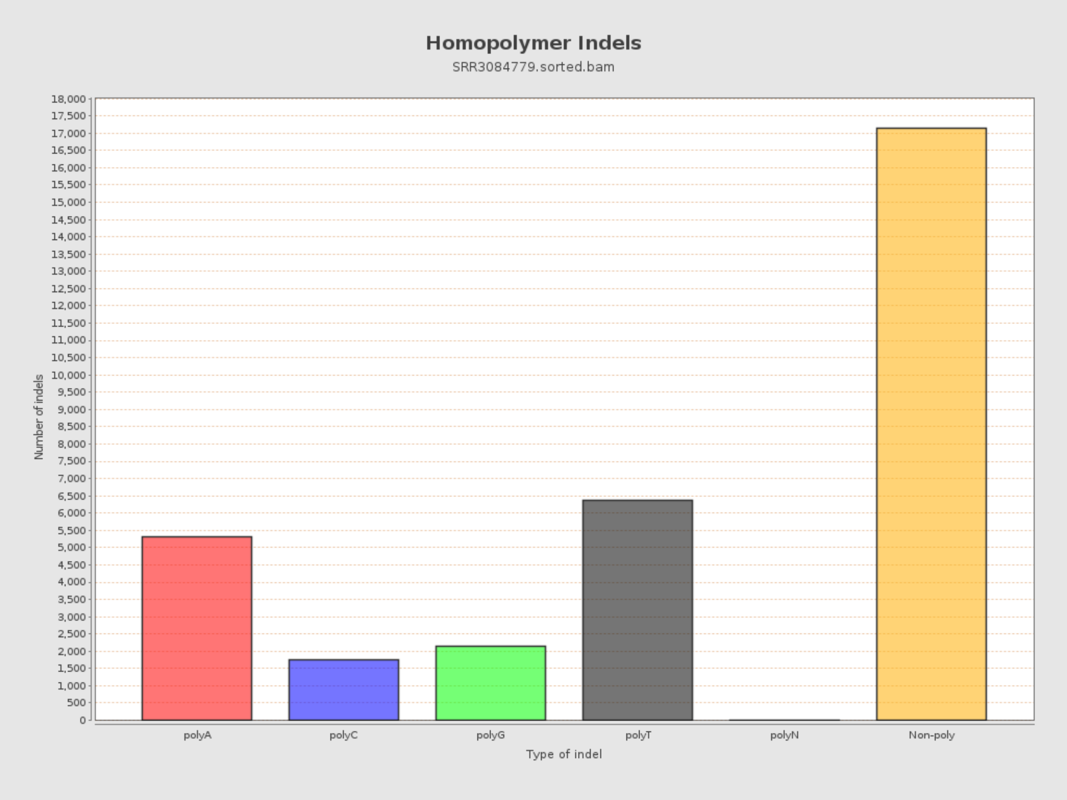
9. Results : Mapped Reads GC-content Distribution



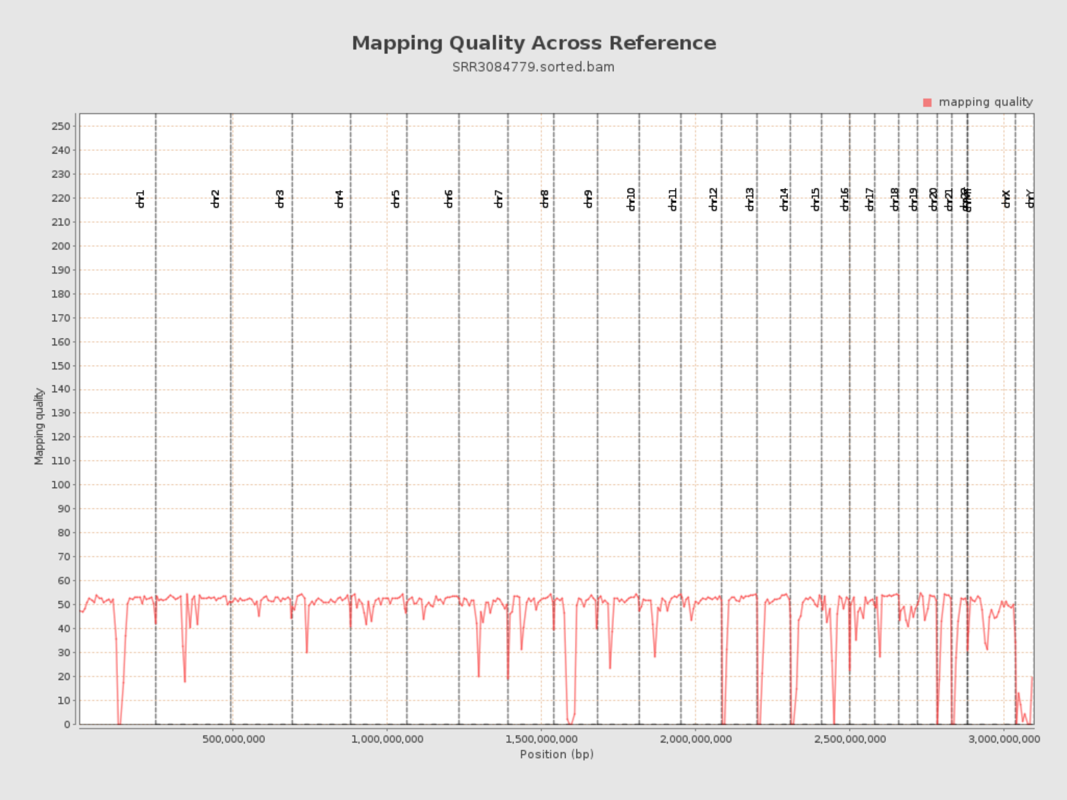
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram